

**AMENDMENTS TO THE CLAIMS:**

Claim 48 is canceled. Claims 33, 35, 37, 38, 39, 40, 47, 58, 59, 60, 62, 63 and 64 are amended. Claim 67 is added. The following is the status of the claims of the above-captioned application, as amended.

33. (Currently amended.) A ~~variant of a parent fungal cutinase variant~~, wherein the variant has above 80% homology to SEQ ID NO:1 and comprises a modification of at least one amino acid residue corresponding to position A4, T29, A88, N91, A130, Q139, I169, I178 or R189 in SEQ ID NO:1; and wherein the variant has cutinase activity.

34. (Previously presented.) The variant claim 33, which comprises the substitution A4V, T29M/I/C, A88H/L/V, N91H, A130V, Q139R, I169A/G/T/V, I178V or R189A/H/V.

35. (Currently amended) The variant of claim 33, wherein the ~~parent cutinase variant~~ is a variant of the cutinase from H. insolens strain DSM 1800.

36. (Canceled.)

37. (Currently amended.) The variant of claim 33, wherein the ~~variant cutinase variant~~ has above 85% homology to SEQ ID NO:1.

38. (Currently amended.) The variant of claim 33, wherein the ~~variant cutinase variant~~ has above 90% homology to SEQ ID NO:1.

39. (Currently amended.) The variant of claim 33, wherein the ~~variant cutinase variant~~ has above 95% homology to SEQ ID NO:1.

40. (Currently amended.) The cutinase variant of claim 33, which further comprises at least one amino acid substitution at a position corresponding to position Q1, L2, E6, G8, E10, S11, A14, N15, A16, F24, V38, N44, L46, E47, S48, H49, R51, D63, L66, S116, S119, G120, L138, T164, T166, L167, I168, L174 and/or E179 in SEQ ID NO:1.

41. (Previously presented.) The variant of claim 33, which variant further comprises at least one amino acid substitution at a position corresponding to Q1P/C/L, L2K/Q/V, E6Q, G8D,

E10Q, S11C/T, A14P, N15T/D, A16T, F24Y, V38H, N44D, L46I, E47K, S48/E/K, H49Y, R51P, D63N, L66I, S116K, S119P, G120D, L138I, T164S, T166M/I, L167P, I168F, L174F and/or E179Qin SEQ ID NO:1.

42. (Previously presented.) The variant of claim 33, which variant further comprises substitutions corresponding to E6Q +A14P +E47K +R51P +E179Qin SEQ ID NO:1.

43. (Previously presented.) The variant of claim 33, which variant has hydrolytic activity towards terephthalic acid esters.

44. (Previously presented.) The variant of claim 33, which variant has hydrolytic activity towards cyclic tri(ethylene terephthalate) and/or Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate.

45. (Previously presented.) The variant of claim 33, which has a denaturation temperature which is at least 5°C higher than the parent cutinase at pH 8.5.

46. (Previously presented.) The variant of claim 41, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Qin SEQ ID NO:1.

47. (Currently amended.) The variant of claim 33, wherein the parent cutinase variant is a variant of a cutinase that has the amino acid sequence of SEQ ID NO:1 and wherein the variant comprises the substitutions corresponding to E6Q +A14P +E47K +R51P +A130V+E179Q.

48. (Cancelled.)

49. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A4.

50. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to T29.

51. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A88.

52. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to N91.

53. (Previously presented.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A130.

54. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to Q139.

55. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to I169.

56. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to I178.

57. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to R189.

58. (Currently amended.) A variant of a parent fungal cutinase variant, wherein the cutinase variant is a variant of a parent cutinase is which is at least 80% homologous to SEQ ID NO:1, wherein the variant differs from the parent cutinase by 1 to 20 substitutions; and wherein said variant and comprises a modification of at least one amino acid residue corresponding to position A4, T29, A88, N91, A130 Q139, I169, I178 or R189 in SEQ ID NO:1; and wherein the variant has cutinase activity.

59. (Currently amended.) A cutinase variant of a parent cutinase, wherein the variant has above 80% homology to SEQ ID NO:1 and comprises a substitution or substitutions selected from the following group of substitutions in SEQ ID NO:1:  
S48E +A88H +N91H +R189V;  
Q1L +L2K +G8D +N15D;

N44D +A130V;  
Q1C +L2V +G120D;  
A88L +R189A;  
S48E +L66I +A88L +I169A +R189H;  
A88V +S116K +S119P +Q139R +I169V +R189V;  
A88V +R189A;  
S48K +A88H +I169G +R189H;  
Q1L +L2Q +A4V +S11T;  
T164S;  
L174F;  
H49Y;  
Q1L +L2K +G8D +N15D +S48E +A88H +N91H +R189V;  
Q1L +L2K +G8D +N15D +N44D +A130V;  
Q1L +L2K +G8D +N15D +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +A16T;  
A130V;  
Q1C +L2V;  
G8D +N15D +A16T;  
G8D +N15D +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +T29M +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +T29I +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +T29C +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +S48E +A88H +N91H +A130V +L174F +I178V +R189V;  
G8D +N15D +S48E +A88H +N91H +A130V +T166M +I168F +R189V;  
G8D +N15D +S48E +A88H +N91H +A130V +T166I +L167P +R189V;  
G8D +N15D +V38H +S48E +A88H +N91H +A130V +I169T +R189V;  
G8D +N15D +V38H +S48E +A88H +N91H +A130V +R189V; and  
G8D +N15D +T29M +S48E +A88H +N91H +A130V +T166I +L167P +R189V;  
and wherein the variant has cutinase activity.

60. (Currently amended.) The variant of claim 59, wherein the parent-cutinase variant is a variant of the cutinase from *H. insolens* strain DSM 1800.

61. (Canceled.)

62. (Currently amended.) The variant of claim 59, wherein the variant-cutinase variant has above 85% homology to SEQ ID NO:1.

63. (Currently amended.) The variant of claim 59, wherein the variant-cutinase variant has above 90% homology to SEQ ID NO:1.

64. (Currently amended.) The variant of claim 59, wherein the variant-cutinase variant has above 95% homology to SEQ ID NO:1.

65. (Previously presented.) The variant of claim 59, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q in SEQ ID NO:1.

66. (Previously presented.) The variant of claim 34, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q in SEQ ID NO:1.